BLAST Searches Performed   ane 23, 1997 (6 page:
HEDRICK, *et al.* USSN: 09/770,528   3)
Atty. Docket No.: DX0725K2B

SPRI/XREFdb BLAST Report xrBLAST4371643066_0

This BLAST Search was run Jun 23 1997 12:47:57

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= IL1EPSILON
        (219 letters)

Database: /data/datasets/nt
           329,017 sequences; 497,918,314 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

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 from this report into SPRI/XREFdb

Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gi|33798|emb|X645...H.sapiens gene for interleukin-1 receptor ant...	0	259	5.8e-05	1
gi|587699|gb|I095...Sequence 1 from Patent WO 8911540	0	239	0.00011	1
gi|587700|gb|I095...Sequence 3 from Patent WO 8911540	0	239	0.00011	1
gi|1008970|emb|X8...H.sapiens mRNA for intracellular IL-1 recepto...	0	239	0.00014	1
gi|587702|gb|I095...Sequence 8 from Patent WO 8911540 >gi|589153|...	0	239	0.00015	1
gi|186291|gb|M556...Human icIL-1ra mRNA, complete cds.	0	239	0.00015	1
gi|186385|gb|M630...Human interleukin 1 receptor antagonist (IL1R...	0	230	0.00031	1
gi|32578|emb|X532...H.sapiens mRNA for IRAP	0	239	0.00036	1
gi|32576|emb|X520...H.sapiens mRNA for interleukin-1 receptor ant...	0	239	0.00037	1
gi|1567289|emb|A3...Synthetic (50Gly,51Gly) IL-1 beta gene	0	206	0.0033	1
gi|1567283|emb|A3...Synthetic IL-1 beta gene	0	206	0.0034	1
gi|1567285|emb|A3...Synthetic (63Ser,65Ser) IL-1beta	0	206	0.0034	1

This BLAST Search was run Jun 23 1997 13:44:40

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= IL1DELTA
        (470 letters)

Database: /data/datasets/nt
        329,017 sequences; 497,918,314 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

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from this report into SPRI/XREFdb

Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gi|545740|gb|S689...sIL-1ra=interleukin-1 receptor antagonist sec...	0	476	1.1e-15	1
gi|425787|dbj|D21...Rabbit mRNA for interleukin 1 receptor antago...	0	467	1.2e-14	1
gi|165436|gb|M575...Rabbit interleukin 1 receptor antagonist (IL1...	0	467	1.2e-14	1
gi|186291|gb|M556...Human icIL-1ra mRNA, complete cds.	0	446	2.4e-14	1
gi|587702|gb|I095...Sequence 8 from Patent WO 8911540 >gi|589153|...	0	446	2.4e-14	1
gi|1008970|emb|X8...H.sapiens mRNA for intracellular IL-1 recepto...	0	446	2.5e-14	1
gi|587699|gb|I095...Sequence 1 from Patent WO 8911540	0	446	2.6e-14	1
gi|587700|gb|I095...Sequence 3 from Patent WO 8911540	0	446	2.6e-14	1
gi|186385|gb|M630...Human interleukin 1 receptor antagonist (IL1R...	0	446	2.7e-14	1
gi|238584|gb|S640...interleukin 1 receptor antagonist protein [mi...	0	442	4.0e-14	1

This BLAST Search was run Jun 23 1997 14:10:53

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= IIIEPSILON
       (219 letters)

Database: /data/datasets/est.
        1,082,928 sequences; 395,818,522 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

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 from this report into SPRI/XREFdb

                         Sequences Producing High Segment
                                  Pairs   Frame Score   P(N)   N

  gi|1497479|gb|AA0...mi08c10.r1 Soares mouse placenta 0   1095   1.2e-43 1
                     4NbMP13.5 14...

  gi|1388557|gb|W78...zd72d01.r1 Soares fetal heart   0   248   2.3e-05 1
                     NbHH19W Homo sa...

  gi|812143|gb|R502...yj58a03.r1 Homo sapiens cDNA   0   229   0.00026 1
                     clone 152908 5' ...

  gi|806268|gb|R468...yj54f05.r1 Homo sapiens cDNA   0   223   0.00052 1
                     clone 152577 5' ...

  gi|2034114|gb|AA3...EST94914 Activated T-cells I   0   183   0.028   1
                     Homo sapiens cDN...

  gi|1693322|gb|AA1...z135f02.r1 Soares pregnant   0   167   0.15   1
                     uterus NbHPU Homo ...

  gi|955649|dbj|D53...Human fetal brain cDNA 5'-end   0   138   0.98   1
                     GEN-119A08.

  gi|944552|gb|R861...yp88b05.r1 Homo sapiens cDNA   0   136   0.998   1
                     clone 194481 5' ...

  gi|1698279|gb|AA1...z102e06.s1 Soares pregnant   0   137   0.9997 1
                     uterus NbHPU Homo ...

  gi|1978267|gb|AA3...EST29113 Cerebellum II Homo   0   131   0.99991 1
                     sapiens cDNA 5' end

gene

gi|35665|emb|X524...H.sapiens DNA for prointerleukin 1beta, exon 7	0	202	0.0038	1
gi|2169701|dbj|E0...Decombinant DNA encoding hybride poly peptide...	0	206	0.0059	1
gi|1567201|emb|A3...Synthetic human IL-1 beta gene	0	200	0.0073	1
gi|1567203|emb|A3...Synthetic human IL-1 beta gene	0	200	0.0073	1
gi|208634|gb|M155...Synthetic human interleukin 1-beta (IL1B) mRN...	0	206	0.0080	1
gi|2169844|dbj|E0...cDNA encoding human interleukin-1	0	206	0.0095	1
gi|1567287|emb|A3...Synthetic (126Ala,128Ala) IL-1 beta gene	0	197	0.010	1
gi|33789|emb|X025...Human mRNA for interleukin 1 beta. Peripheral...	0	206	0.010	1
gi|2168898|dbj|E0...cDNA encoding human interleukin-1	0	206	0.010	1
gi|208636|gb|M350...Human growth hormone/interleukin 1-beta fusio...	0	200	0.010	1
gi|313969|gb|I002...Sequence 2 from Patent US 4898818	0	206	0.011	1
gi|514106|emb|A21...pGIF- alpha	0	206	0.011	1
gi|2169489|dbj|E0...cDNA encoding a polypeptide,GIF precursor hav...	0	206	0.011	1
gi|313921|gb|I011...Sequence 1 from Patent US 4762914	0	206	0.011	1
gi|35662|emb|X560...Human mRNA for prointerleukin 1 beta.	0	206	0.011	1
gi|186268|gb|K027...Human monocyte interleukin 1 (IL-1) mRNA, com...	0	206	0.011	1
gi|186287|gb|M549...Human monocyte interleukin mRNA, complete cds.	0	206	0.011	1
gi|186283|gb|M153...Human interleukin 1-beta (IL1B) mRNA, complet...	0	206	0.011	1
gi|589345|gb|I079...Sequence 1 from Patent EP 0161901	0	206	0.011	1
gi|2169107|dbj|E0...cDNA sequence for human IL-1	0	206	0.011	1
gi|269368|gb|I007...Sequence 2 from Patent US 4766069	0	206	0.011	1
gi|186281|gb|M158...Human interleukin 1-beta (IL1B) gene, complet...	0	203	0.019	1
gi|33788|emb|X045...Human gene for prointerleukin 1	0	202	0.022	1

This BLAST Search was run Jun 23 1997 14:05:26

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= FF1DELTA
        (470 letters)

Database: /usr/users/gcgdata/gcgblastest
        888,004 sequences; 326,874,798 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

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 from this report into SPRI/XREFdb

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
GB_EST7:W08205...W08205 mb49b11.r1 Soares mouse p3NMF19.5 Mus ...		0	1410	7.1e-58	1
GB_EST8:W78043...W78043 zd72d01.r1 Soares fetal heart NbHH19W ...		0	439	4.5e-14	1
GB_EST7:W20594...W20594 mc16c06.r1 Soares mouse p3NMF19.5 Mus ...		0	400	3.2e-12	1
GB_EST2:R50241...R50241 yj58a03.r1 Homo sapiens cDNA clone 152...		0	395	6.7e-12	1
GB_EST2:R46871...R46871 yj54f05.r1 Homo sapiens cDNA clone 152...		0	385	2.1e-11	1
GB_EST7:W13935...W13935 mb23a07.r1 Soares mouse p3NMF19.5 Mus ...		0	149	0.96	1

[Entrez][Return to the top of this page]

>GB_EST7:W08205 W08205 mb49b11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA
        clone 332733 5' similar to PIR:A49031 A49031 interleukin 1
receptor
        antagonist - mouse ;. 9/96
        Length = 382

```
   gi|198389|gb|M631...M.musculus interleukin 1          0     442   4.2e-14 1
                      receptor antagonist ...

   gi|204928|gb|M631...Rat interleukin 1 receptor        0     433   1.0e-13 1
                      antagonist gene, c...
   gi|32578|emb|X532...H.sapiens mRNA for IRAP           0     446   1.2e-13 1 ···

   gi|32576|emb|X520...H.sapiens mRNA for interleukin-1  0     446   1.2e-13 1
                      receptor ant...

   gi|198298|gb|M575...Mouse interleukin 1 receptor      0     442   1.7e-13 1
                      antagonist (IL1R...

   gi|198387|gb|M742...Mouse IL-1rn antagonist protein   0     442   1.9e-13 1
                      mRNA, complet...

   gi|198296|gb|M644...Mus domesticus interleukin 1      0     442   2.0e-13 1
                      receptor antagon...

   gi|1313894|gb|L38...Sus scrofa (clone p0328w) IRAP1   0     397   4.1e-12 1
                      mRNA, complet...

   gi|33798|emb|X645...H.sapiens gene for interleukin-1  0     392   5.6e-11 1
                      receptor ant...

   gi|487864|gb|L328...Mouse germline interleukin 1      0     379   2.1e-10 1
                      receptor antagon...

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[Entrez][Return to the top of this page]

>gi|545740|gb|S68977|S68977 sIL-1ra=interleukin-1 receptor antagonist secreted
            form [rabbits, colon tissue, mRNA, 574 nt]
            Length = 574

  Plus Strand HSPs:

  Score = 476 (71.4 bits), Expect = 1.1e-15, P = 1.1e-15
  Identities = 196/283 (69%), Positives = 196/283 (69%), Strand = Plus / Plus

Query:    147 GGCACTGGATGCCAGTCTGTCCCCTGTCATCCTGGGCGTTCA-AGGAGGAAGCCAGTGCC 205
                  G C CT GA GCC   TC G C CCTGT  TCCTGGGC T CA AGG GGAAG    GTGCC
Sbjct:    255 GCCCCTTGA-GCC--TCAG-CTCCTGT--TCCTGGGCATCCAGAGGGGGAAGTT-GTGCC 307

Query:    206 TATCTTGTGGGA---CAGAGAA-AGGGCCAATTCTGAAACTTGAGCCAGTGAACATCATG 261
                  T TCTTGTG GA    C G G A AG   AA CT A  T GAG C GT AACATCA
Sbjct:    308 TGTCTTGTGTGAAGTCTGGGGATAAGATGAAG-CTCCATTTGGAGGCCGTTAACATCACT 366

Query:    262 GAGCTCTACCTCGGGGCCAAGGA--ATCA-AAGAGCTTCACCTTCTACCGGCGGGATATG 318
                  GA C CT   C G  CAAGGA  A  A AAG GCTTCACCTTC  CCG      ATA
Sbjct:    367 GA-C-CTGGG-CAAGAACAAGGAGCAGGACAAGCGCTTCACCTTCATCCGCTCCAATAGT 423

Query:    319 GGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTCCTCTGCACCTCACCG 378
                  GG C TACC CCA CTTCGA TC GC  CCT CCC GGCTGGTT CTCTGCAC  C C G
Sbjct:    424 GGCCCTACCACCACCTTCGAGTCTGCCTCCTGCCCGGGCTGGTTTCTCTGCACGGCCCTG 483

Query:    379 GAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCCGCC-TGG 429
                  GA GCTGACCAGCC GTCAG CTCAC  A A CCC GA GAC CC  C TGG
Sbjct:    484 GAGGCTGACCAGCCGGTCAGCCTCACCAACACCCCGGACGACTCCATCGTGG 535

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SPRI/XREFdb BLAST Report xrBLAST1048889160_0

This BLAST Search was run Sep 9 1997 18:00:45 ε

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query=   (219 letters)

Database: /data/datasets/nt
           349,525 sequences; 540,957,745 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gi|33798|emb|X64532|HSIL1RECA	H.sapiens gene for interleukin-1 receptor ant...	0	259	6.3e-05	1
gi|2303331|emb|A50276|A50276	Sequence 10 from Patent WO9612022	0	239	7.3e-05	1
gi|2303056|emb|A49726|A49726	Sequence 1 from Patent WO9609323 >gi|2303291|...	0	239	0.00011	1
gi|587699|gb|I09591|	Sequence 1 from Patent WO 8911540	0	239	0.00012	1
gi|587700|gb|I09592|	Sequence 3 from Patent WO 8911540	0	239	0.00012	1
gi|1008970|emb|X84348|HSIL1RAII	H.sapiens mRNA for intracellular IL-1 recepto...	0	239	0.00015	1
gi|2303333|emb|A50279|A50279	Sequence 13 from Patent WO9612022	0	239	0.00015	1
gi|587702|gb|I09594|	Sequence 8 from Patent WO 8911540 >gi|589153|...	0	239	0.00016	1
gi|186291|gb|M55646|HUMIL1RAA	Human icIL-1ra mRNA, complete cds.	0	239	0.00016	1
gi|186385|gb|M63099|HUMILRA	Human interleukin 1 receptor antagonist (IL1R...	0	230	0.00034	1
gi|32578|emb|X53296|HSI1RAP	H.sapiens mRNA for IRAP	0	239	0.00039	1
gi|32576|emb|X52015|HSI1RA	H.sapiens mRNA for interleukin-1 receptor ant...	0	239	0.00040	1
gi|1567289|emb|A32118|A32118	Synthetic (50Gly,51Gly) IL-1 beta gene	0	206	0.0036	1
gi|1567283|emb|A32000|A32000	Synthetic IL-1 beta gene	0	206	0.0037	1

This BLAST Search was run Sep 9 1997 17:56:23

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query=   (470 letters)

Database: /data/datasets/nt
          349,525 sequences; 540,957,745 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gil545740lgblS68977lS68977	sIL-1ra=interleukin-1 receptor antagonist sec...	0	476	1.2e-15	1
gil425787ldbjlD21832lRABI1RA1	Rabbit mRNA for interleukin 1 receptor antago...	0	467	1.3e-14	1
gil165436lgblM57526lRABIL1RAB	Rabbit interleukin 1 receptor antagonist (IL1...	0	467	1.3e-14	1
gil186291lgblM55646lHUMIL1RAA	Human icIL-1ra mRNA, complete cds.	0	446	2.6e-14	1
gil587702lgblI09594l	Sequence 8 from Patent WO 8911540 >gil589153l...	0	446	2.6e-14	1
gil2303333lemblA50279lA50279	Sequence 13 from Patent WO9612022	0	446	2.7e-14	1
gil1008970lemblX84348lHSIL1RAII	H.sapiens mRNA for intracellular IL-1 recepto...	0	446	2.7e-14	1
gil587699lgblI09591l	Sequence 1 from Patent WO 8911540	0	446	2.9e-14	1
gil587700lgblI09592l	Sequence 3 from Patent WO 8911540	0	446	2.9e-14	1
gil186385lgblM63099lHUMILRA	Human interleukin 1 receptor antagonist (IL1R...	0	446	2.9e-14	1
gil2303056lemblA49726lA49726	Sequence 1 from Patent WO9609323 >gil2303291l...	0	446	2.9e-14	1
gil2303331lemblA50276lA50276	Sequence 10 from Patent WO9612022	0	446	3.3e-14	1
gil238584lgblS64082lS64082	interleukin 1 receptor antagonist protein [mi...	0	442	4.3e-14	1

gi|198389|gb|M63100|MUSILRA	M.musculus interleukin 1 receptor antagonist ...	0	442	4.5e-14	1
gi|204928|gb|M63101|RATILRA	Rat interleukin 1 receptor antagonist gene, c...	0	433	1.1e-13	1
gi|32578|emb|X53296|HSI1RAP	H.sapiens mRNA for IRAP	0	446	1.3e-13	1
gi|32576|emb|X52015|HSI1RA	H.sapiens mRNA for interleukin-1 receptor ant...	0	446	1.3e-13	1
gi|198298|gb|M57525|MUSIL1RAA	Mouse interleukin 1 receptor antagonist (IL1R...	0	442	1.8e-13	1
gi|198387|gb|M74294|MUSILIRN	Mouse IL-1rn antagonist protein mRNA, complet...	0	442	2.1e-13	1
gi|198296|gb|M64404|MUSIL1RA	Mus domesticus interleukin 1 receptor antagon...	0	442	2.1e-13	1
gi|1313894|gb|L38849|PIGIRAP	Sus scrofa (clone p0328w) IRAP1 mRNA, complet...	0	397	4.5e-12	1
gi|33798|emb|X64532|HSIL1RECA	H.sapiens gene for interleukin-1 receptor ant...	0	392	6.1e-11	1
gi|487864|gb|L32838|MUSIL1RN	Mouse germline interleukin 1 receptor antagon...	0	379	2.2e-10	1

[Entrez] [Return to the top of this page]

>gi|545740|gb|S68977|S68977 sIL-1ra=interleukin-1 receptor antagonist secreted
          form [rabbits, colon tissue, mRNA, 574 nt]
          Length = 574

  Plus Strand HSPs:

  Score = 476 (71.4 bits), Expect = 1.2e-15, P = 1.2e-15
  Identities = 196/283 (69%), Positives = 196/283 (69%), Strand = Plus / Plus

Query: 147 GGCACTGGATGCCAGTCTGTCCCCTGTCATCCTGGGCGTTCA-AGGAGGAAGCCAGTGCC 205
             G C CT GA GCC   TC G C CCTGT   TCCTGGGC T CA AGG GGAAG   GTGCC
Sbjct: 255 GCCCCTTGA-GCC--TCAG-CTCCTGT--TCCTGGGCATCCAGAGGGGGAAGTT-GTGCC 307

Query: 206 TATCTTGTGGGA---CAGAGAA-AGGGCCAATTCTGAAACTTGAGCCAGTGAACATCATG 261
             T TCTTGTG GA   C G GAA G AA CT A T GAG C GT AACATCA
Sbjct: 308 TGTCTTGTGTGAAGTCTGGGGATAAGATGAAG-CTCCATTTGGAGGCCGTTAACATCACT 366

Query: 262 GAGCTCTACCTCGGGGCCAAGGA--ATCA-AAGAGCTTCACCTTCTACCGGCGGGATATG 318
             GA C CT   C G CAAGGA A A AAG GCTTCACCTTC CCG   ATA
Sbjct: 367 GA-C-CTGGG-CAAGAACAAGGAGCAGGACAAGCGCTTCACCTTCATCCGCTCCAATAGT 423

Query: 319 GGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTCCTCTGCACCTCACCG 378
             GG C TACC CCA CTTCGA TC GC CCT CCC GGCTGGTT CTCTGCAC C C G
Sbjct: 424 GGCCCTACCACCACCTTCGAGTCTGCCTCCTGCCCGGGCTGGTTTCTCTGCACGGCCCTG 483

Query: 379 GAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCCGCC-TGG 429
             GA GCTGACCAGCC GTCAG CTCAC A CCC GA GAC CC C TGG
Sbjct: 484 GAGGCTGACCAGCCGGTCAGCCTCACCAACACCCCGGACGACTCCATCGTGG 535

This BLAST Search was run Sep 9 1997 20:09:02

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query=   △   (470 letters)

Database: /data/datasets/est
          1,182,287 sequences; 435,520,876 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gi|1282415|gb|W08205|W08205	mb49b11.r1 Soares mouse p3NMF19.5 Mus musculu...	0	1410	9.4e-58	1
gi|1388557|gb|W78043|W78043	zd72d01.r1 Soares fetal heart NbHH19W Homo sa...	0	439	5.9e-14	1
gi|1297494|gb|W20594|W20594	mc16c06.r1 Soares mouse p3NMF19.5 Mus musculu...	0	400	4.2e-12	1
gi|812143|gb|R50241|R50241	yj58a03.r1 Homo sapiens cDNA clone 152908 5' ...	0	395	8.9e-12	1
gi|806268|gb|R46871|R46871	yj54f05.r1 Homo sapiens cDNA clone 152577 5' ...	0	385	2.7e-11	1
gi|1287978|gb|W13935|W13935	mb23a07.r1 Soares mouse p3NMF19.5 Mus musculu...	0	149	0.99	1

[Entrez][Build a Contig][Return to the top of this page]

>gi|1282415|gb|W08205|W08205 mb49b11.r1 Soares mouse p3NMF19.5 Mus musculus
          cDNA clone 332733 5' similar to PIR:A49031 A49031 interleukin 1
          receptor antagonist - mouse ;
          Length = 382

  Plus Strand HSPs:

 Score = 1410 (211.6 bits), Expect = 9.4e-58, P = 9.4e-58
 Identities = 282/282 (100%), Positives = 282/282 (100%), Strand = Plus / Plus